



SEQUENCE LISTING

<110> KLOEK, Andrew P.
Williams, Deryck Jeremy
Salmon, Brandy

<120> NEMATODE GS-LIKE SEQUENCES

<130> 12557-004001

<140> US 10/098,602

<141> 2002-03-15

<150> US 60/276,621

<151> 2001-03-16

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<170> FastSEQ for Windows Version 4.0

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<211> 1471

<212> DNA

<213> Meloidogyne incognita

<220>

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Leu Asn Asn Leu Ile Arg Asn Gly Lys Ile Asp Thr Val Val Leu Ala
10 15 20

tgc gtc gac atg caa ggc cgg ctg atg ggc aag aga tta act ggg cgt 150
Cys Val Asp Met Gln Gly Arg Leu Met Gly Lys Arg Leu Thr Gly Arg
25 30 35

cat ttt tta gga ttg gat caa aag aag att agc att agc acg ttt gta 198
His Phe Leu Gly Leu Asp Gln Lys Lys Ile Ser Ile Ser Thr Phe Val
40 45 50 55

tat gcg gta act ata gaa ggc atc gct ggc gga ggt tat gag atc tca 246
Tyr Ala Val Thr Ile Glu Gly Ile Ala Gly Gly Tyr Glu Ile Ser
60 65 70

agt gta gac aca ggt tat agt gat tgt cat ctc tgt gca gat ttg aat 294
Ser Val Asp Thr Gly Tyr Ser Asp Cys His Leu Cys Ala Asp Leu Asn
75 80 85

tcc ctt cat tta ctc ccg tgg tca gaa ggc gct gta ttg gca att tcc 342
Ser Leu His Leu Leu Pro Trp Ser Glu Gly Ala Val Leu Ala Ile Ser

90	95	100	
aat cct cat aat ttc gtt act tct gag cca ttg ttc tgt tct cct cga Asn Pro His Asn Phe Val Thr Ser Glu Pro Leu Phe Cys Ser Pro Arg 105 110 115			390
gtt atg ctc atg cag caa att gag cgc ctg gct aat cta aag ctt aaa Val Ile Leu Met Gln Gln Ile Glu Arg Leu Ala Asn Leu Lys Leu Lys 120 125 130 135			434
ggc ctt ttt gct tct gaa cta gaa ttt aat ctt ttc aac gaa act tat Gly Leu Phe Ala Ser Glu Leu Glu Phe Asn Leu Phe Asn Glu Thr Tyr 140 145 150			486
aag agt gcc agc caa aag cat tgg aaa aat tta aaa acc gcg cag cct Lys Ser Ala Ser Gln Lys His Trp Lys Asn Leu Lys Thr Ala Gln Pro 155 160 165			534
cat cat caa tgg atg aat att agt gca agt agt ggg att gaa act ttt His His Gln Trp Met Asn Ile Ser Ala Ser Ser Gly Ile Glu Thr Phe 170 175 180			582
atg cgt tct gtg cgt aat aaa tta gaa gaa gcc ggt att ctg atg gag Met Arg Ser Val Arg Asn Lys Leu Glu Glu Ala Gly Ile Leu Met Glu 185 190 195			630
ggc aca cat ccc gaa ttt tta cct ayt cag cat gaa ctt aat ttt gta Ala Thr His Pro Glu Phe Leu Pro Ser Gln His Glu Leu Asn Phe Val 200 205 210 215			676
cca gcc gat cct cta aca atg gca gat cgt cat att att gca aaa cat Pro Ala Asp Pro Leu Thr Met Ala Asp Arg His Ile Ile Ala Lys His 220 225 230			726
gga gtt cgc gaa atg gca gaa cag tct gga atg gtt gca act ttt atg Gly Val Arg Glu Met Ala Glu Gln Ser Gly Met Val Ala Thr Phe Met 235 240 245			774
gtt aaa ttg ayt tca act gcg ctt gyt aat gcc tgg cat att cat atg Ala Lys Leu Ser Ser Thr Ala Leu Gly Asn Ala Cys His Ile His Met 250 255 260			822
tca ctt caa gat gca gaa aca gaa aaa aat gca ttt tat dat caa dac Ser Leu Gln Asp Ala Glu Thr Glu Lys Asn Ala Phe Tyr Asp Gln Asn 265 270 275			870
gat gaa tat gga atg tca acc tta gct cgt aat tgg att gct gga tta Asp Glu Tyr Gly Met Ser Thr Leu Ala Arg Asn Trp Ile Ala Gly Leu 280 285 290 295			918
ttg aaa tac gta cct gaa gcg act tat ttc ttt gca tct tac atc dac Leu Lys Tyr Val Pro Glu Ala Thr Tyr Phe Phe Ala Ser Tyr Ile Asn 300 305 310			966
tcc tac aaa aga ctt caa ccg ctt ayt ttt gcg cca aca aaa tgt tgt Ser Tyr Lys Arg Leu Gln Pro Leu Thr Phe Ala Pro Thr Lys Cys Cys 315 320 325			1014

tgg gca att gac aac cga aca agc gcc ttt cga ctt tgt aat tca aaa Trp Ala Ile Asp Asn Arg Thr Ser Ala Phe Arg Leu Cys Asn Ser Lys 330 335 340	1062
tcc gag gga att aat gtt gag ctg cgt att ggt ggc gct gat ttg aac Ser Glu Gly Ile Asn Val Glu Leu Arg Ile Gly Gly Ala Asp Leu Asn 345 350 355	1119
cct tat tta gct ttt tcc gca atc ata gct gca gga att agc ggt ata Pro Tyr Leu Ala Phe Ser Ala Ile Ile Ala Ala Gly Ile Ser Gly Ile 360 365 370 375	1156
gaa gaa aag ctt gaa ctt ccc cct cct gca tat ggc aat gtt taa aat Glu Glu Lys Leu Glu Leu Pro Pro Pro Ala Ser Gly Asn Val Tyr Asn 380 385 390	1206
gat aag gaa tta cct gaa ttt cct aat tcc tta caa aat gct aca cat Asp Lys Glu Leu Pro Glu Phe Pro Asn Ser Leu Gln Asn Ala Thr His 395 400 405	1254
cct cta aaa gaa tgg aaa atg ctg aat aaa aca ttc ggg gag aag ttg Leu Leu Lys Glu Ser Lys Met Leu Asn Lys Thr Phe Gly Glu Lys Leu 410 415 420	1302
att cta cat tat gta aac gct gct aat gtt gag att aat gaa ttt tca Ile Leu His Tyr Val Asn Ala Ala Asn Val Glu Ile Asn Glu Phe Ser 425 430 435	1350
aaa caa gtt act gac tgg gag ctt aat caa gga ttt aat aga tat Lys Glu Val Thr Asp Trp Glu Leu Asn Glu Gly Phe Asn Arg Tyr 440 445 450	1395
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Ile Asp Thr Val Val Leu Ala Cys Val Asp Met Gln Gly Arg Leu Met 20 25 30	
Gly Lys Arg Leu Thr Gly Arg His Phe Leu Gly Leu Asp Gln Lys Lys 35 40 45	
Ile Ser Ile Ser Thr Phe Val Tyr Ala Val Thr Ile Glu Gly Ile Ala 50 55 60	
Gly Gly Gly Tyr Glu Ile Ser Ser Val Asp Thr Gly Tyr Ser Asp Cys 65 70 75 80	
His Leu Cys Ala Asp Leu Asn Ser Leu His Leu Leu Pro Trp Ser Glu 85 90 95	
Gly Ala Val Leu Ala Ile Ser Asn Pro His Asn Phe Val Thr Ser Glu 100 105 110	
Pro Leu Phe Cys Ser Pro Arg Val Ile Leu Met Gln Gln Ile Glu Arg	

115	120	125
Leu Ala Asn Leu Lys Leu Lys Gly Leu Phe Ala Ser Glu Leu Glu Phe		
130	135	140
Asn Leu Phe Asn Glu Thr Tyr Lys Ser Ala Ser Gln Lys His Trp Lys		
145	150	155
Asn Leu Lys Thr Ala Gln Pro His His Gln Trp Met Asn Ile Ser Ala		
165	170	175
Ser Ser Gly Ile Glu Thr Phe Met Arg Ser Val Arg Asn Lys Leu Gln		
180	185	190
Glu Ala Gly Ile Leu Met Glu Ala Thr His Pro Glu Phe Leu Pro Ser		
195	200	205
Gln His Glu Leu Asn Phe Val Pro Ala Asp Pro Leu Thr Met Ala Asp		
210	215	220
Arg His Ile Ile Ala Lys His Gly Val Arg Glu Met Ala Glu Gln Ser		
225	230	235
Gly Met Val Ala Thr Phe Met Ala Lys Leu Ser Ser Thr Ala Leu Gly		
245	250	255
Asn Ala Cys His Ile His Met Ser Leu Gln Asp Ala Glu Thr Glu Lys		
260	265	270
Asn Ala Phe Tyr Asp Gln Asn Asp Glu Tyr Gly Met Ser Thr Leu Ala		
275	280	285
Arg Asn Trp Ile Ala Gly Leu Leu Lys Tyr Val Pro Glu Ala Thr Tyr		
290	295	300
Phe Phe Ala Ser Tyr Ile Asn Ser Tyr Lys Arg Leu Gln Pro Leu Thr		
305	310	315
Phe Ala Pro Thr Lys Cys Cys Trp Ala Ile Asp Asn Arg Thr Ser Ala		
325	330	335
Phe Arg Leu Cys Asn Ser Lys Ser Gln Gly Ile Asn Val Glu Leu Arg		
340	345	350
Ile Gly Gly Ala Asp Leu Asn Pro Tyr Leu Ala Phe Ser Ala Ile Ile		
355	360	365
Ala Ala Gly Ile Ser Gly Ile Glu Glu Lys Leu Glu Leu Pro Pro Pro		
370	375	380
Ala Ser Gly Asn Val Tyr Asn Asp Lys Glu Leu Pro Glu Phe Pro Asn		
385	390	395
Ser Leu Gln Asn Ala Thr His Leu Leu Lys Glu Ser Lys Met Leu Asn		
405	410	415
Lys Thr Phe Gly Glu Lys Leu Ile Leu His Tyr Val Asn Ala Ala Asn		
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Gln Gly Phe Asn Arg Tyr		
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<212> DNA

<213> Meloidogyne incognita

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gaaggcatcg ctggcgagg ttatgagatc tcaagtgtag acacaggta tagtggatgt	240
cattctgtcg cagatttgaa ttcccttcat ttactcccgt ggtcagaagg cgctgttattg	300
gcaatttcca atcctcataaa ttctgttaact tctgagccat ttgttgttc tcctcgagta	360
atactcatgc agcaaattga ggcctggct aatctaaagc ttaaaggct ttttgcct	420

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aatttaaaaa	cccgccagc	tcatcatcaa	tggatgaata	tttagtcaag	tagtgggatt	540
gaaactttt	tgcgttctgt	gcgtataaaa	ttagaagaag	ccggattttt	gatggaggcg	600
acacatccc	aatttttacc	tagtcagcat	gaactaat	ttgtaccags	cgatcttata	660
aaatggcag	atcgicatat	tattjaaaaa	catggagtt	jcgaaatggc	agaacagtct	720
ggaatggtt	caacttttat	ggctaaattt	agttcaactg	cggttggtaa	tgcctgcata	780
attcatatgt	caattcaaga	tgcagaaaca	gaaaaaaaaatq	cattttatga	tcaaaaacgt	840
gaatatggaa	tgtcaasett	agctgtata	tggattgtcg	gattattgaa	atasgtacat	900
giagcgactt	atttttttg	atottacato	aactgtgtca	aaagacttca	accgttact	960
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aattcaaaaat	ccgagggaaat	taatjtttgag	ctgctgtattt	gtggcgttga	tttgaacccct	1080
tatttagctt	tttcggcaat	catajgtgtca	ggaatttageg	gtataagaaga	aaagcttgaa	1140
cttcgcctc	ctgcatctgg	caatgtttac	aatgtataagg	aattacctga	atttcctaata	1200
ttcttacaaa	atgtctacaca	tctttaaaaa	gsatcgasaa	tgttgaataa	aacatcgogg	1260
gagaagggtga	ttctacatta	tgtaaacgt	gtataatgttj	agattaatga	attttcaaaa	1320
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111-457

4-12, P.F.T

<213 · *Mycobacterium tuberculosis*

430 - 4

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Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val
35 40 45

Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala
50 55 60

Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp
 70 75 80 85 90

Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu

Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu

100 105 110

Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu

115 120 125
Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val

130 135 140
Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala

145 150 155 160
Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile

165 170 175
Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp

180 185 190

Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Iys

195 200 205
Gly Glu Cys Asp Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu

Ala Leu Val Thr Cys Asp Asp His Ile Ile Tyr Lys Asp Gly Ala Lys

Ald Ser Val Thr Asp Asp His His Ala Thr Tyr Bys Asp Gly Ala S₃
 225 230 235 240
 Glu Ile Ala Asp Glu His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr

Asp-Gly-Ala-Asp-Gln-His-Ser-Lys-Ser-Lys-Tyr-Met-Ala-Lys-Tyr
245 250 255

Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gl
260 265 270

Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met
 275 . 280 285
 Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg
 290 295 300
 Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe
 305 310 315 320
 Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn
 325 330 335
 Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val
 340 345 350
 Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala
 355 360 365
 Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu
 370 375 380
 Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg
 385 390 395 400
 Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala
 405 410 415
 Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
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22

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